

Temporal variation in loggerhead turtle strandings from Georgia

Final Report to Georgia Department of Natural Resources

Prepared by

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## INTRODUCTION

Marine turtles utilize different habitats throughout their developmental stages. Knowledge of the origin of animals in different habitats can benefit management by providing information as to which populations may be impacted by human activities. Stranded turtles offer an opportunity to gather information on the populations of turtles that inhabit or travel through different coastal areas. The relative ease of collection of tissue samples also affords researchers the opportunity to test temporal variation in marine turtle cohorts. For example, does the demographic composition of stranded turtles vary seasonally or from year to year?

Loggerhead turtles were previously sampled by stranding network volunteers in 1997 to determine the nesting populations that contribute individuals to Georgian coastal waters. The initial sampling in 1997 provided evidence that at least two nesting populations contribute individuals at detectable levels to the stranded cohort in Georgia (Bass et al., 1998). We also quantified sampling errors in both the mixture (stranded cohort) and stock (nesting populations) samples which affects the precision of contribution estimates from potential source populations.

Samples were collected in 1998 to enhance the sample size and to determine if temporal variation in the stranded cohort could be detected. Investigations in other species of marine turtles have indicated that there is a temporal component to the demographic composition of populations at particular foraging locations (Bass et al., unpubl. data). Because there is some sharing of haplotypes among nesting locations, it is not possible to assign *individuals* to a given location. The maximum likelihood programs that are currently being used generate the most likely contributions of source populations based on the haplotype frequencies in the stocks and the mixture. The ability of these programs to find the correct answer is based on several assumptions. The most important assumption is that all potential source populations have been characterized and that there are strong shifts in haplotype frequencies in these source populations (Pella and Milner, 1987). Another assumption is that the mixture has been sampled in a manner sufficient to capture the real diversity of haplotypes present in the foraging or stranded population. Investigations into the stock structure of fish have shown that increases in sample size can provide several benefits, such as a reduction in the standard errors of frequency estimates for common haplotypes and an increase in the probability of detecting rare “endemic” haplotypes which in turn increases resolution (Epifanio et al., 1995). Due to the predominance of haplotypes A and B (haplotypes found in the majority of nesting locations used in this analysis) in the 1997 sample and the low frequency of endemic haplotypes, an increase in the sample size of the stranded turtles was desirable to determine if our sampling was a sufficient estimate of the genetic diversity of stranded loggerheads in Georgia.

## METHODS

Tissue samples were collected by Sea Turtle Stranding Network volunteers and placed in 15 ml of saturated salt preservation buffer. Samples were then transferred to the University of Florida for analysis. Standard phenol/chloroform DNA isolation protocols were conducted on the tissue samples and a 380 bp fragment of the mitochondrial DNA control region was amplified using primers designed for sea turtles (Allard et al., 1994; Norman et al., 1994). Individual fragments were sequenced and compared to known *Caretta caretta* nesting beach haplotypes. Individuals were then assigned a haplotype based on designations from Encalada et al. (1998) and Bolten et al. (1998).

To test for statistical differences among haplotype frequencies between years, chi-square analyses were performed with the program CHIRXC (Zaykin and Pudovkin, 1993) and probabilities were generated using a Monte Carlo randomization procedure (Roff and Bentzen, 1989).

Maximum likelihood (ML) analysis for mixed stock identification (Grant et al., 1980) was used to estimate the contributions of nesting populations to foraging habitat in Georgia. This method estimates the most likely contributions of source populations based on the haplotype frequencies in the source populations and in the mixed population. The maximum likelihood programs GIRLSEM and UCON were used (Masuda et al., 1991). As a starting point in ML iterations using GIRLSEM, it was assumed that all source populations had an equal probability of contributing (i.e. population size, distance from the foraging location, etc. did not have an impact on the percentage of animals recruiting to a particular area). The conditional maximum likelihood estimates from GIRLSEM were then used as the initial guess to generate a point estimate in the unconditional maximum likelihood program, UCON. Standard errors and 95% confidence intervals of the point estimates were generated from 100 bootstraps of the stock and mixture data sets using GIRLSEM (see Pella et al., 1998).

## RESULTS AND DISCUSSION

### *DNA Analysis of 1998 samples*

Of the 124 samples collected, 108 samples produced readable sequence and 16 samples did not work, indicating technical difficulties in the recovery of DNA sequencing information. In the sample of 108 individuals, haplotypes A and B were the most common (Table 1). Six of the haplotypes found during the 1997 sampling period were seen in 1998, but an additional 2 haplotypes (E and J) were found in the 1998 sample. Haplotype E has been observed in the South Florida nesting population while haplotype J has been observed in Mexico. One individual in both the 1997 and 1998 sample sets carried haplotype M (Table 1). In the 1998 set of samples, four individuals which possess haplotype N were found. Haplotypes M and N still remain unknown as to their origin. In addition, four individuals had haplotypes not previously observed at surveyed nesting localities or foraging locations. These were designated GA-1 to GA-4 (see Appendix 1). Although several different haplotypes were found in the second sample represented by the 1998 group, the haplotype frequencies of the two years were not significantly different from each other ( $X^2 = 10.20$ ,  $P = 0.341$ ).

Table 1. Haplotype composition and frequency of stranded loggerhead turtle samples from 1998 and 1997 and locations where these haplotypes have been observed. See Appendix 1 for a detailed listing of haplotypes by turtle or incident number.

<i>Haplotype</i>	<i>1998</i>	<i>1997</i>	<i>Location</i>
			<i>Nesting<sup>1</sup></i>
<b>A</b>	56	51	NWFL, SFL, NEFL-NC
<b>B</b>	33	35	NWFL, SFL, NEFL-NC, Mexico, Greece
<b>C</b>	4	6	NWFL, SFL, Mexico
<b>E</b>	2	0	SFL
<b>G</b>	2	1	NWFL, SFL
<b>J</b>	2	0	Mexico
	(n = 99)	(n = 93)	<i>Foraging<sup>2</sup> or Stranded<sup>3</sup></i>
<b>K</b>	0	1	Madeira <sup>2</sup>
<b>M</b>	1	1	Azores <sup>2</sup>
<b>N</b>	4	6	Azores <sup>2</sup> , Madeira <sup>2</sup> , North Atlantic Coast <sup>3</sup>
<b>GA-1</b>	1	0	Georgia <sup>4</sup>
<b>GA-2</b>	1	0	Georgia <sup>4</sup>
<b>GA-3</b>	1	0	Georgia <sup>4</sup>
<b>GA-4</b>	1	0	Georgia <sup>4</sup>
	Total = 108	Total = 101	

<sup>1</sup> Abbreviations according to Encalada et al. (1998): NWFL = northwest Florida (panhandle region), SFL = southeast and southwest Florida, NEFL-NC = northeast Florida to North Carolina.

<sup>2</sup> Bolten et al. (1998), <sup>3</sup> Rankin-Baransky et al. (submitted), <sup>4</sup> This study.

### Maximum Likelihood Analysis

Due to the non-significant difference of the haplotype frequencies between the two sampling periods (1997 & 1998), the samples from both years were combined to estimate the contributions of potential source populations (Table 2). This analysis once again provided evidence that SFL contributes the majority of individuals that strand along the Georgia coast. In addition, the nesting population in NWFL was again implicated as a contributor to the stranded turtle cohorts in Georgia.

Table 2. Maximum likelihood estimates of contribution by source populations to stranded loggerhead cohorts from both 1997 and 1998 (n = 192). Estimates were generated using UCON. Standard errors and 95% confidence intervals were generated from 100 bootstraps of both the stock and mixture using GIRLSEM.

<i>Source population</i>	<i>Contribution (PE)</i>	<i>S.E.</i>	<i>95% C.I.</i>
NWFL	0.1999	0.1975	0.1607-0.2391
SFL	0.6623	0.2028	0.6221-0.7025
NEFL-NC	0.1049	0.1269	0.0797-0.1301
MEXICO	0.0327	0.0340	0.0259-0.0667
BRAZIL	0	0	
GREECE	0.0000	0.0854	0.0000-0.0169

The ML analysis yielded a notably large estimate (0.1999) from Northwest Florida (Table 2). We believe this result was an overestimate due to in part to the frequency of individuals with haplotype C in the Georgia stranded cohort. After some discussion, we concluded that the estimated contribution from the Florida panhandle (NWFL) was not biologically realistic. Nesting effort in this area may include 100-200 turtles annually (Meylan et al. 1995), as compared to tens of thousands of turtles that nest in southern Florida. Hence the panhandle is an important nesting area, but probably too small to detect with precision in ML analyses. Based on these considerations, we provisionally removed the NWFL rookery from the analysis (Table 3).

Table 3. Maximum likelihood estimates of contribution by source populations to stranded loggerhead cohorts from both 1997 and 1998 (n = 192). The source population NWFL, was removed from the analysis. Estimates were generated using UCON. Standard errors and 95% confidence intervals were generated from 100 bootstraps of both the stock and mixture using GIRLSEM.

<i>Source Population</i>	<i>Contribution (PE)</i>	<i>S.E.</i>	<i>95% C.I.</i>
SFL	0.7274	0.1499	0.6977-0.7571

NEFL-NC	0.2392	0.1098	0.2174-0.2610
MEXICO	0.0334	0.0455	0.0246-0.0422
BRAZIL	0.0000	0.0000	
GREECE	0.0000	0.0541	0.0000-0.0107

Removal of NWFL as a potential source population reduces the standard error about the mean for all source populations except Mexico (Table 3). In addition, these estimates appear to be more reflective of population sizes and proximity of nesting populations to the Georgia coastal area. These two factors have been identified as potential determinants of foraging ground composition in green turtles (Bass and Witzell, 2000; Lahanas et al., 1998).

We feel that the estimates of contribution listed in Table 3 are the best estimates for the Georgia stranding cohort.

## CONCLUSIONS

### *Temporal Variation*

There is no significant difference among haplotype frequencies from strandings in 1997 ( $n = 101$ ) and 1998 ( $n = 108$ ). The main difference between the two sampling years is the presence or absence of low-frequency haplotypes. For example, we observed several rare haplotypes in 1998 that were not detected in 1997, notably haplotypes E and J. Even though we are using a program that attempts to compensate for small sample sizes in some categories (Roff and Bentzen, 1989), the limitations of the Chi-square test may prohibit the detection of subtle differences. We conclude that there are no detectable differences between the 1997 and 1998 stranding cohorts, but this does not eliminate the possibility of temporal variation on longer timescales, or during periods of climatic fluctuation. Sampling from year to year may be too short a time frame to detect temporal variation in loggerheads. Hence it may be useful to reexamine stranded cohorts from Georgia in 5 to 10 years.

### *Demographic Composition and Comparison to Atlantic Foraging Populations*

Our initial analysis yielded an anomalously high contribution from the Florida panhandle. Given the small size of this rookery (Meylan et al. 1995), the estimate of 19% was biologically unrealistic. Subsequent reanalysis without the panhandle population yielded results with lower standard errors. We support the results of this analysis (Table 3) as a basis for management decisions. However, the problem with overestimates from small nesting colonies deserves further attention. One strong possibility is that we have not adequately sampled the genetic variation in regional nesting colonies.

We can state with strong support that a large proportion of the stranded loggerheads are from the south Florida nesting populations. This was apparent in the analysis of samples

from 1997 (77%) and here in the analysis of the combined data set (73%; Table 3). The increased sample size did capture more of the diversity of loggerheads utilizing Georgia waters. The presence of haplotype J also prompted an estimated contribution of 3% from Mexico. Although the standard error is still high and we should be cautious in interpreting this estimate, there do appear to be Mexican loggerheads utilizing US coastal waters.

Investigations of the genetic composition of stranded loggerheads along the northeast coast of the US indicated that 59% were from SFL, 25% from NEFL-NC, and 16% from Mexico (Rankin-Baransky et al., 1999). Notably there was no evidence of a contribution from the NWFL population and the contribution of the SFL population was lower than what we estimate here for the Georgia stranding cohorts. The NC foraging population from Core Sound also exhibits a similar composition: 64% from SFL, 32% from NEFL-NC, and the remaining 4% divided among Mexico and Brazil (Bass et al., 1997). Our estimates for the Georgia stranded cohorts corroborate general conclusions from these other studies. Most strandings along the Atlantic seaboard originate from the SFL nesting population, followed by contributions from NEFL-NC and Yucatan (Mexico). It is likely that other nesting areas contribute at low frequency, but were not detected with current samples and limits of resolution.

Previous research on green turtles, *Chelonia mydas*, has indicated that both nesting population size (Lahanas et al., 1998) and distance from the nesting population to the foraging location (Bass and Witzell, 2000) are correlated with relative contributions to feeding populations. Differences between loggerhead foraging populations may be associated with either of these factors or there may be other unquantified determinants of foraging population composition (Bass and Witzell, 2000).

### Management Implications

The estimated composition of the Georgia stranding cohort indicates that several nesting populations may be affected by coastal activities in Georgia. A high proportion of loggerheads derived from the SFL management unit are using Georgian waters as a migratory pathway or resident feeding habitat. In addition about a quarter of the stranded cohort are derived from the NEFL-NC management unit with the remaining proportion composed of animals derived from the Mexican nesting locality. Other diminutive or unsurveyed populations in the Atlantic (such as those in Northwest Florida, the Bahamas, or Cuba) may be affected as well.

What are the management implications for the Georgia nesting population? In the ML analysis, the Georgia nesting population is combined with those in South Carolina, North Carolina, and northeastern Florida (Amelia Island), because we lack the resolution to distinguish these nesting areas with current mtDNA assays. (Forthcoming microsatellite surveys may alleviate this problem.) Hence we cannot give an exact contribution of the Georgia nesting population to the Georgia strandings. However, it is reasonable to assume that Georgia contributes to the 21-26% estimate from NEFL-NC at a level proportional to the size of this nesting population.

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## Appendix 1. Distribution of haplotypes in stranded individuals

Lab #	Stranding ID #	Location	Haplotype
<b>SAMPLES FROM 1997</b>			
915	CR-97060601-CC-CI	Georgia; Cumberland Island	B
916	CR-97053003-CC-CI	Georgia; Cumberland Island	N
917	CR-97070101-CC-CI	Georgia; Cumberland Island	B
918	CR-97062601-CC-CI	Georgia; Cumberland Island	N
919	CR-97072102-CC-CI	Georgia; Cumberland Island	A
920	CR-97081001-CC-CI	Georgia; Cumberland Island	A
921	CR-97072501-CC-CI	Georgia; Cumberland Island	B
922	CR-97060503-CC-CI	Georgia; Cumberland Island	B
923	CR-97050901-CC-CI	Georgia; Cumberland Island	B
924	CR-97053001-CC-CI	Georgia; Cumberland Island	B
925	CR-97062702-CC-CI	Georgia; Cumberland Island	A
926	CR-97081201-CC-CI	Georgia; Cumberland Island	A
927	CR-97081301-CC-CI	Georgia; Cumberland Island	A
928	CR-97091401-CC-CI	Georgia; Cumberland Island	A
929	CR-97060604-CC-CI	Georgia; Cumberland Island	A
930	CR-97051701-CC-CI	Georgia; Cumberland Island	B
931	CR-97060402-CC-CI	Georgia; Cumberland Island	A
932	CR-97060401-CC-CI	Georgia; Cumberland Island	B
933	CR-97092202-CC-CI	Georgia; Cumberland Island	A
934	CR-97092401-CC-CI	Georgia; Cumberland Island	B
935	CR-97100301-CC-CI	Georgia; Cumberland Island	G
936	CR-97052501-CC-CI	Georgia; Cumberland Island	B
937	CR-97052902-CC-CI	Georgia; Cumberland Island	B
938	CR-97062401-CC-CI	Georgia; Cumberland Island	B
939	CR-97062801-CC-CI	Georgia; Cumberland Island	B
940	CR-97072301-CC-CI	Georgia; Cumberland Island	B
941	CR-97060502-CC-CI	Georgia; Cumberland Island	A
942	CR-97072101-CC-CI	Georgia; Cumberland Island	A
943	CR-97051703-CC-CI	Georgia; Cumberland Island	B
944	CR-97062603-CC-CI	Georgia; Cumberland Island	B
945	CR-97042604-CC-CI	Georgia; Cumberland Island	C
946	CR-97062703-CC-CI	Georgia; Cumberland Island	A
947	CR-97061901-CC-CI	Georgia; Cumberland Island	A
948	CR-97072201-CC-CI	Georgia; Cumberland Island	A
949	CR-97062402-CC-CI	Georgia; Cumberland Island	A
950	CR-97052502-CC-CI	Georgia; Cumberland Island	B
951	CR-97060501-CC-CI	Georgia; Cumberland Island	A
952	CR-97071301-CC-CI	Georgia; Cumberland Island	B
953	CR-97071601-CC-CI	Georgia; Cumberland Island	A
954	CR-97092101-CC-CI	Georgia; Cumberland Island	A
955	CR-97061902-CC-CI	Georgia; Cumberland Island	B
956	CR-97063003-CC-CI	Georgia; Cumberland Island	B
957	CR-97052303-CC-CI	Georgia; Cumberland Island	A
958	CR-97062501-CC-CI	Georgia; Cumberland Island	C
959	CR-97052801-CC-CI	Georgia; Cumberland Island	A
960	CR-97063002-CC-CI	Georgia; Cumberland Island	A

Lab #	Stranding ID #	Location	Haplotype
961	CR-97050101-CC-CI	Georgia; Cumberland Island	A
962	CR-97052301-CC-CI	Georgia; Cumberland Island	A
963	CR-97060603-CC-CI	Georgia; Cumberland Island	B
964	CR-97100102-CC-CI	Georgia; Cumberland Island	A
965	CR-97092201-CC-CI	Georgia; Cumberland Island	A
966	CR-97052503-CC-CI	Georgia; Cumberland Island	A
967	CR-97051301-CC-CI	Georgia; Cumberland Island	A
968	CR-97070102-CC-CI	Georgia; Cumberland Island	A
969	CR-97062606-CC-CI	Georgia; Cumberland Island	M
970	CR-97082401-CC-CI	Georgia; Cumberland Island	A
971	CR-97051702-CC-CI	Georgia; Cumberland Island	A
972	CR-97052302-CC-CI	Georgia; Cumberland Island	A
973	CR-97053002-CC-CI	Georgia; Cumberland Island	A
974	CR-97062701-CC-CI	Georgia; Cumberland Island	N
975	CR-97062605-CC-CI	Georgia; Cumberland Island	B
976	CR-97081801-CC-CI	Georgia; Cumberland Island	B
977	GA-97052201	Georgia; JEK	N
978	GA-97071403	Georgia; JEK	B
979	GA-97092302	Georgia; JEK	B
980	GA-97092301	Georgia; JEK	B
981	GA-97071401	Georgia; JEK	B
982	GA-97060501	Georgia; JEK	A
983	GA-97080802	Georgia; JEK	NW
984	GA-97081201	Georgia; JEK	A
985	GA-97061701	Georgia; JEK	NW
986	GA-97071201	Georgia; JEK	NW
987	GA-97071402	Georgia; JEK	N
988	GA-97051501	Georgia; JEK	NW
989	GA-97080801	Georgia; JEK	B
990	GA-97052401	Georgia; SAP	C
991	GA-970701001	Georgia; SAP	B
992	GA-97090901	Georgia; SAP	A
993	GA-970701601	Georgia; SAP	A
994	GA-97052301	Georgia; SAP	B
995	GA-97062401	Georgia; Sea Island	A
996	GA-97070302	Georgia; Sea Island	A
997	GA-97070601	Georgia; Sea Island	A
998	GA-97042401	Georgia; Sea Island	B
999	GA-97063001	Georgia; Sea Island	A
1000	GA-97072301	Georgia; Sea Island	A
1001	GA-97062901	Georgia; Sea Island	B
1002	GA-97070301	Georgia; Sea Island	K
1003	GA-97071301	Georgia; St. Simons Island	B
1004	GA-97050801	Georgia; St. Simons Island	A
1005	GA-97090101	Georgia; St. Simons Island	C
1006	GA-97062601	Georgia; St. Simons Island	A

Lab #	Stranding ID #	Location	Haplotype
1007	GA-97050801	Georgia **	NW
1008	GA-97050601	Georgia **	NW
1009	GA-97070201	Georgia **	C
1010	GA-97052501	Georgia **	A
1011	GA-97052001	Georgia; OSS	NW
1012	GA-97062301	Georgia; OSS	N
1013	GA-97052401	Georgia; OSS	B
1014	GA-97070201	Georgia; OSS	A
1015		Georgia; SCI	NW
1016	GA-9708071	Georgia; SCI	NW
1017	GA-9706131	Georgia; SCI	C
1018	GA-97052601	Georgia; SCI	A
1019	GA-97051401	Georgia; LSS	A
1020	GA-9706091	Georgia; LSS	A
1021	GA-97070901	Georgia; LSS	A
1022	GA-97082001	Georgia; LSS	B
1023	GA-97060601	Georgia; LSS	NW
1024	GA-97070601	Georgia; LSS	A
1025	GA-97052801	Georgia; LSS	A
<b>SAMPLES FROM 1998</b>			
1863	GA98091501	GA; Tybee Isl	B
1864	GA98070501	GA; Cumberland Isl	J
1865	GA98071301	GA; Tybee Isl	B
1866	GA98082001	GA; Tybee Isl	A
1867	GA98101101	GA; Little Cumberland Isl	NW
1868	GA98060301	GA; Little Cumberland Isl	B
1869	GA98062501	GA; Sapelo Isl	A
1870	GA98070301	GA; Sapelo Isl	J
1871	GA98063001	GA; Sapelo Isl	A
1872	GA98072201	Ga; Saint Simons Isl	B
1873	GA98062801	Ga; Saint Simons Isl	B
1874	GA98091101	Ga; Saint Simons Isl	B
1875	GA98070101	GA; Sea Isl	GA-1
1876	GA98061401	GA; Sea Isl	A
1877	GA98051902	GA; Saint Catherine's Isl	B
1878	GA98061101	GA; Sea Isl	C
1879	GA98062201	GA; Sea Isl	A
1880	GA98081001	GA; Sea Isl	B
1881	GA98050601	GA; Jekyll Isl	B
1882	GA98050101	GA; Jekyll Isl	B
1883	GA98080602	GA; Jekyll Isl	GA-2
1884	GA98092401	GA; Tybee Isl	B
1885	GA98052401	GA; Jekyll Isl	B
1886	GA98060601	GA; Tybee Isl	B
1887	GA98062702	GA; Jekyll Isl	A
1888	GA98062701	GA; Jekyll Isl	A

Lab #	Stranding ID #	Location	Haplotype
1889	GA98052901	GA; Jekyll Isl	B
1890	GA98052902	GA; Jekyll Isl	A
1891	GA98040601	GA; Jekyll Isl	B
1892	GA98090901	GA; Jekyll Isl	A
1893	GA98051101	GA; Jekyll Isl	A
1894	GA98053001	GA; Jekyll Isl	A
1895	GA98051401	GA; Jekyll Isl	A
1896	GA98062501	GA; Saint Catherine's Isl	A
1897	GA98052901	GA; Ossabaw Isl	NW
1898	GA98071801	GA; Ossabaw Isl	B
1899	GA98051901	GA; Ossabaw Isl	NW
1900	GA98082001	GA; Ossabaw Isl	GA-3
1901	GA98070901	GA; Ossabaw Isl	NW
1902	GA98060901	GA; Ossabaw Isl	A
1903	GA98052401	GA; Ossabaw Isl	B
1904	GA98060801	GA; Ossabaw Isl	A
1905	GA98063001	GA; Ossabaw Isl	NW
1906	GA98083102	GA; Ossabaw Isl	NW
1907	GA98092701	GA; Cumberland Isl	B
1908	GA98080401	GA; Cumberland Isl	A
1909	GA98092401	GA; Cumberland Isl	A
1910	GA98061101	GA; Cumberland Isl	N
1911	GA98051901	GA; Cumberland Isl	M
1912	GA98070901	GA; Saint Catherine's Isl	A
1913	GA98062801	GA; Cumberland Isl	A
1914	GA98072102	GA; Cumberland Isl	N
1915	GA98062304	GA; Cumberland Isl	A
1916	GA98080402	GA; Cumberland Isl	A
1917	GA98070601	GA; Cumberland Isl	G
1918	GA98091601	GA; Cumberland Isl	A
1919	GA98060903	GA; Cumberland Isl	B
1920	GA98070602	GA; Cumberland Isl	A
1921	GA98061801	GA; Cumberland Isl	A
1922	GA98071301	GA; Cumberland Isl	B
1923	GA98071301	GA; Saint Catherine's Isl	A
1924	GA98072101	GA; Cumberland Isl	A
1925	GA98072301	GA; Saint Catherine's Isl	A
1926	GA98071001	GA; Cumberland Isl	A
1927	GA98070604	GA; Cumberland Isl	A
1928	GA98111203	GA; Cumberland Isl	B
1929	GA98062301	GA; Cumberland Isl	A
1930	GA98071201	GA; Cumberland Isl	A
1931	GA98060102	GA; Cumberland Isl	A
1932	GA98072301	GA; Cumberland Isl	A
1933	GA98061201	GA; Cumberland Isl	B
1934	GA98062101	GA; Cumberland Isl	NW

Lab #	Stranding ID #	Location	Haplotype
1935	GA98052001	GA; Cumberland Isl	A
1936	GA98110901	GA; Cumberland Isl	A
1937	GA98070801	GA; Cumberland Isl	A
1938	GA98042901	GA; Cumberland Isl	B
1939	GA98061001	GA; Cumberland Isl	NW
1940	GA98062203	GA; Cumberland Isl	A
1941	GA98100101	GA; Cumberland Isl	E
1942	GA98091101	GA; Cumberland Isl	C
1943	GA98062502	GA; Cumberland Isl	A
1944	GA98062305	GA; Cumberland Isl	A
1945	GA98060901	GA; Cumberland Isl	N
1946	GA98053101	GA; Cumberland Isl	G
1947	GA98043002	GA; Cumberland Isl	NW
1948	GA98082101	GA; Cumberland Isl	A
1949	GA98062303	GA; Cumberland Isl	B
1950	GA98050701	GA; Cumberland Isl	A
1951	GA98092402	GA; Cumberland Isl	GA-4
1952	GA98062204	GA; Cumberland Isl	A
1953	GA98062802	GA; Cumberland Isl	A
1954	GA98031601	GA; Cumberland Isl	B
1955	GA98060905	GA; Cumberland Isl	E
1956	GA98053102	GA; Cumberland Isl	A
1957	GA98060904	GA; Cumberland Isl	A
1958	GA98072202	GA; Cumberland Isl	B
1959	GA98062701	GA; Cumberland Isl	C
1960	GA98052101	GA; Cumberland Isl	B
1961	GA98060902	GA; Cumberland Isl	A
1962	GA98051402	GA; Cumberland Isl	A
1963	GA98062302	GA; Cumberland Isl	B
1964	GA98041601	GA; Cumberland Isl	NW
1965	GA98040202	GA; Cumberland Isl	C
1966	GA98053001	GA; Cumberland Isl	A
1967	GA98062202	GA; Cumberland Isl	A
1968	GA98043001	GA; Cumberland Isl	NW
1969	GA98073001	GA; Cumberland Isl	A
1970	GA98073002	GA; Cumberland Isl	A
1971	GA98060104	GA; Cumberland Isl	B
1972	GA98051403	GA; Cumberland Isl	B
1973	GA98082001	GA; Jekyll Isl	A
1974	GA98072401	GA; Ossabaw Isl	A
1975	GA98051903	GA; Saint Catherine's Isl	B
1976	GA97052401	GA; Tybee Isl	A
1977	GA98060101	GA; Sant Catherine's Isl	NW
1978	GA98072302	GA; Blackbeard Isl	B
1979	GA98101001	GA; Blackbeard Isl	NW
1980	GA98053002	GA; Blackbeard Isl	A

<b>Lab #</b>	<b>Stranding ID #</b>	<b>Location</b>	<b>Haplotype</b>
1981	GA98053001	GA; Blackbeard Isl	B
1982	GA98081701	GA; Blackbeard Isl	N
1983	GA98072301	GA; Blackbeard Isl	A
1984	GA98053101	GA; Blackbeard Isl	NW
1985	GA98062601	GA; Blackbeard Isl	NW
1986	GA98060101	GA; Wassaw Isl	NW

NW= Not Working